

FIG. 1

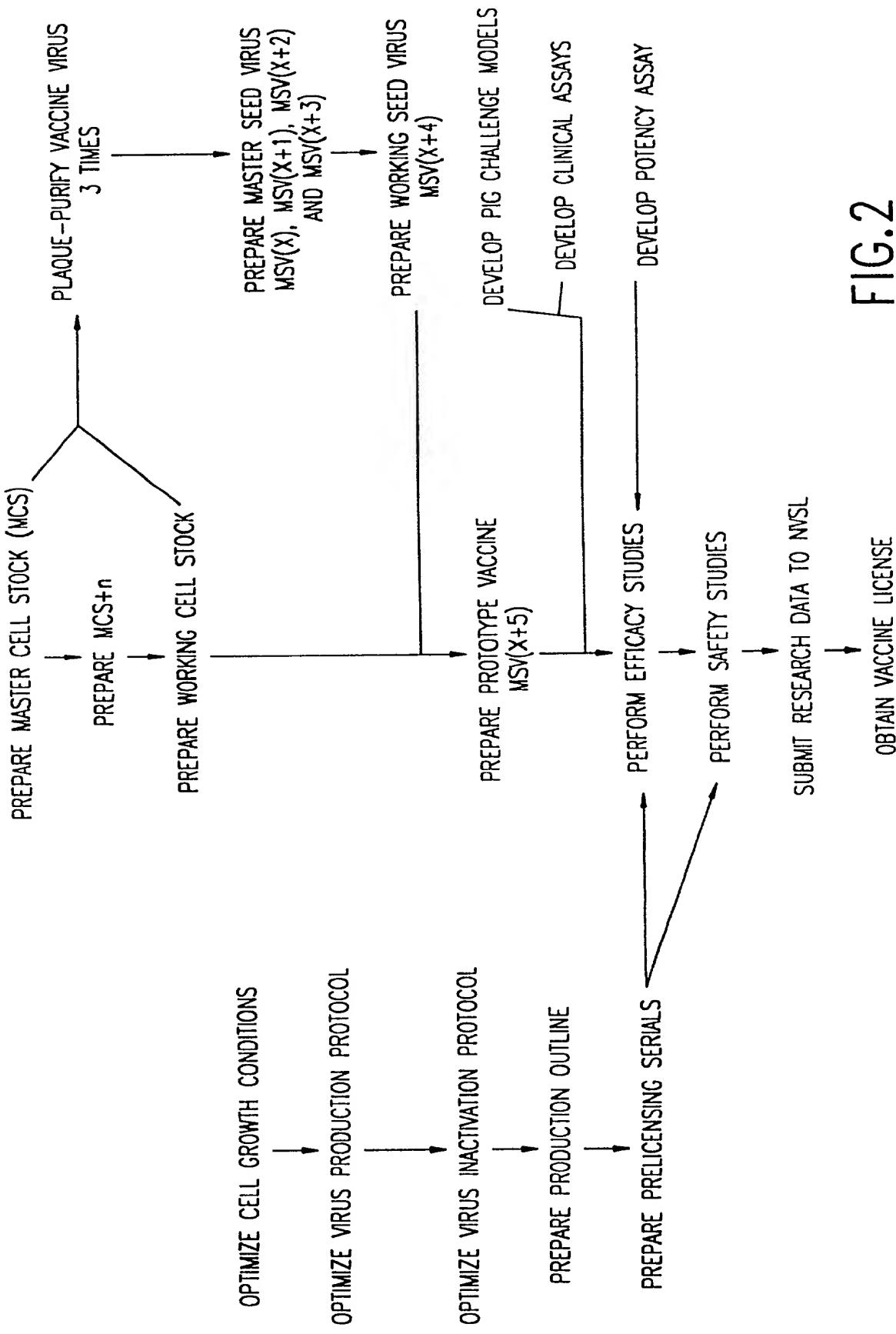


FIG. 2

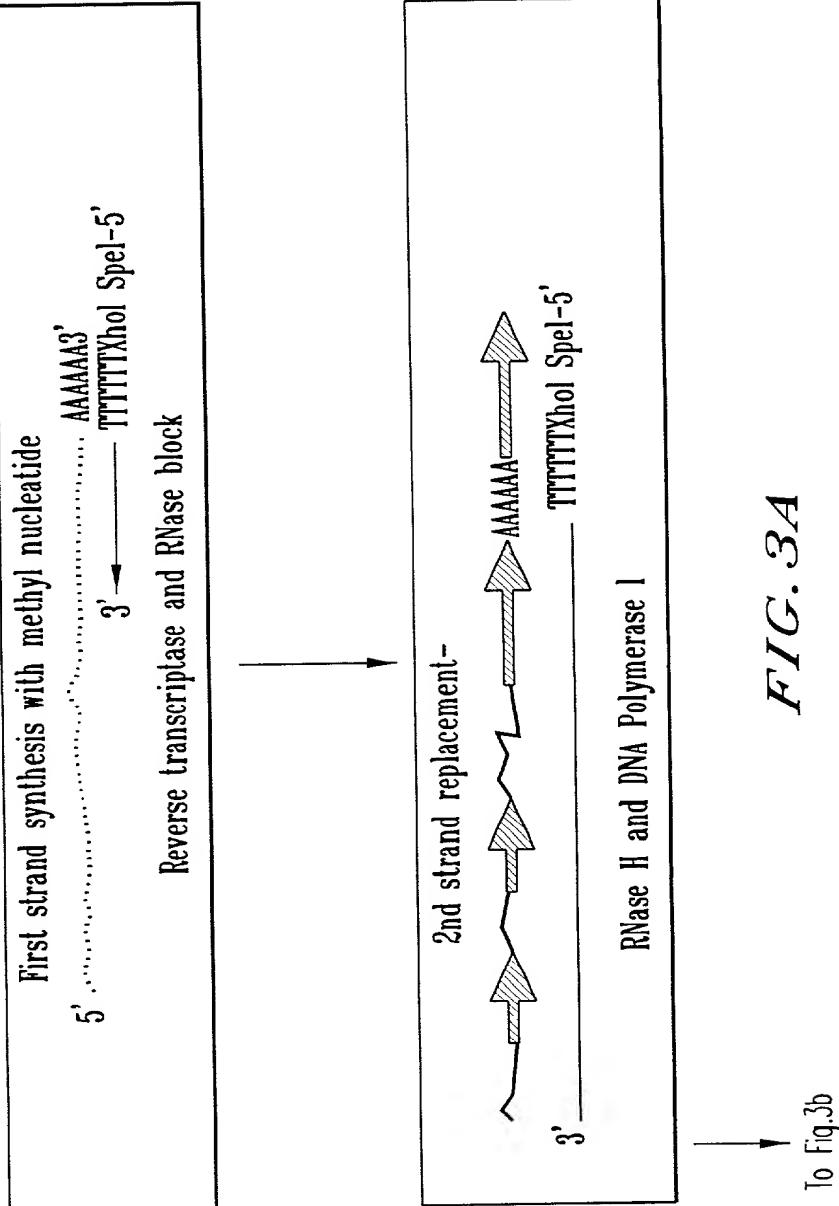


FIG. 3A

To Fig. 3b

From Fig.3a

PHENOL EXTRACT AND
ETHANOL PRECIPITATE DNA

Blunting-DNA endas
Xhol SpeI
T4 DNA Pol

Phenol
extract
precipitate

Rl adaptor
Xhol SpeI
Rl adaptor

T4 DNA ligase

Heat-inactivate
ligase

Kinase adaptors
T4 Polynucleotide kinase

Xhol digest

Separate Xho I digested cDNA on Sephadex G-400 column

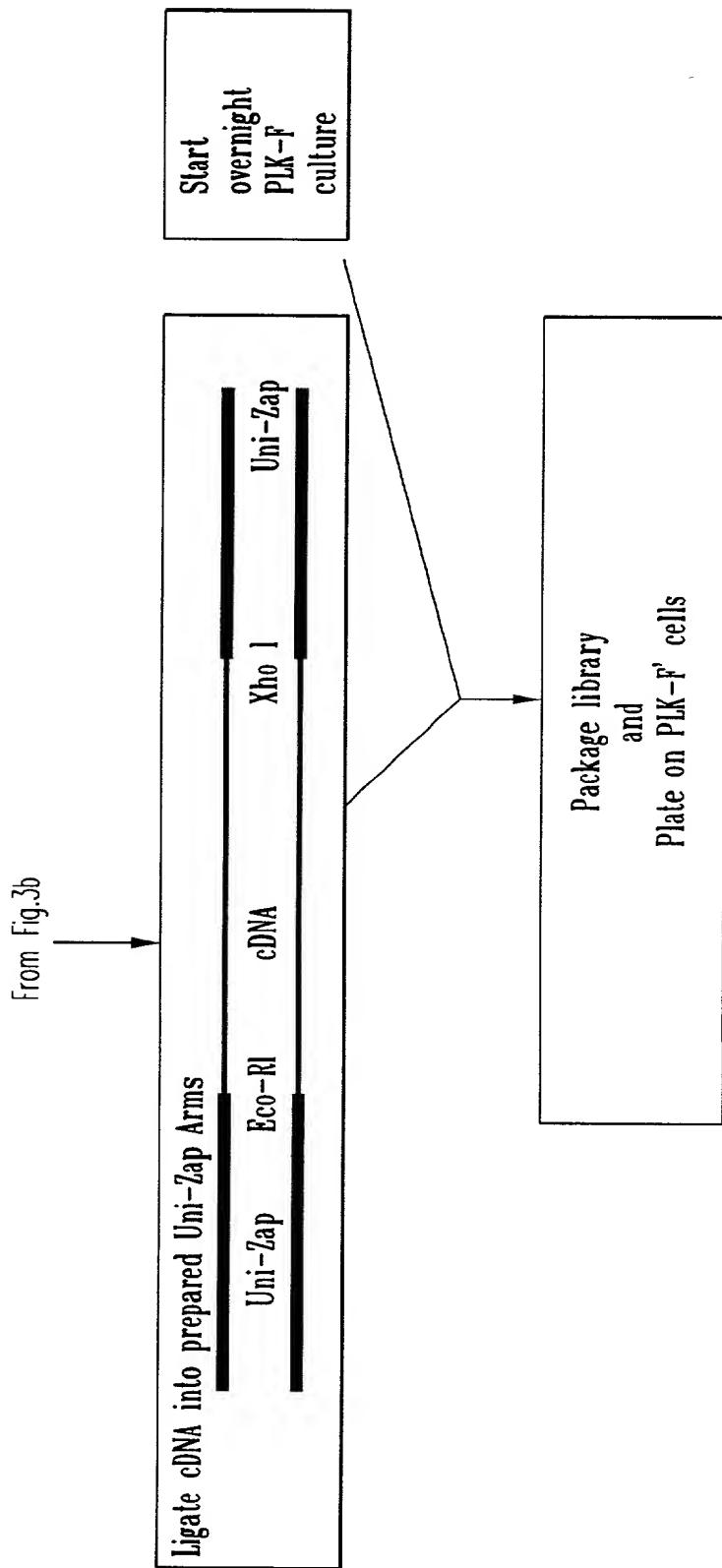
5'Eco RI

Xho I

To Fig.3c

FIG. 3B

FIG. 3c



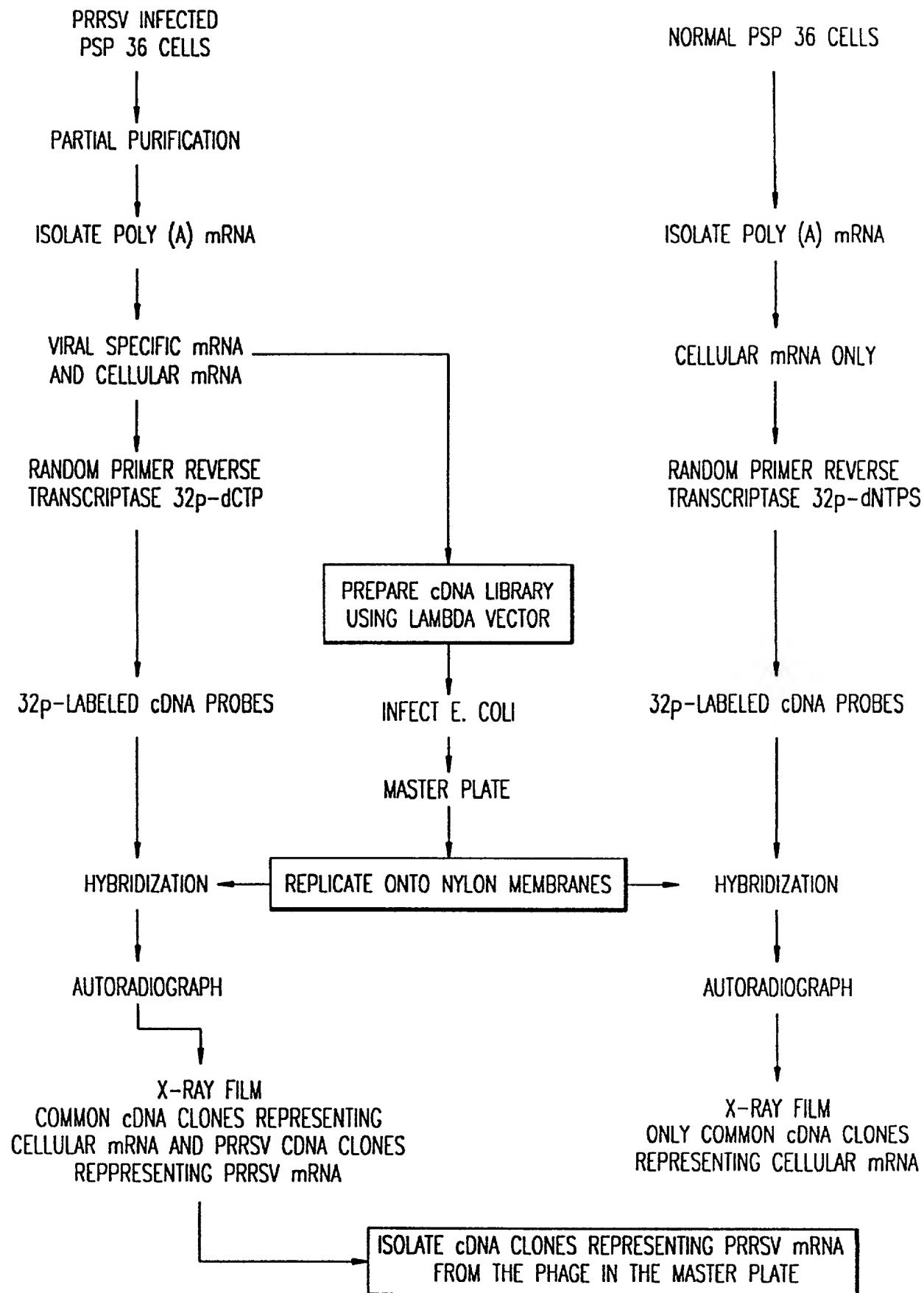


FIG.4

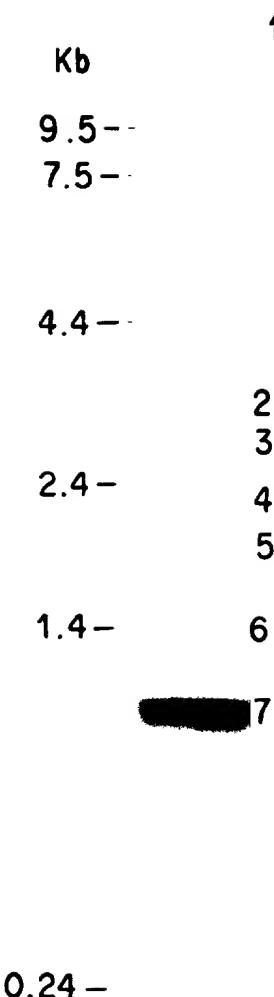
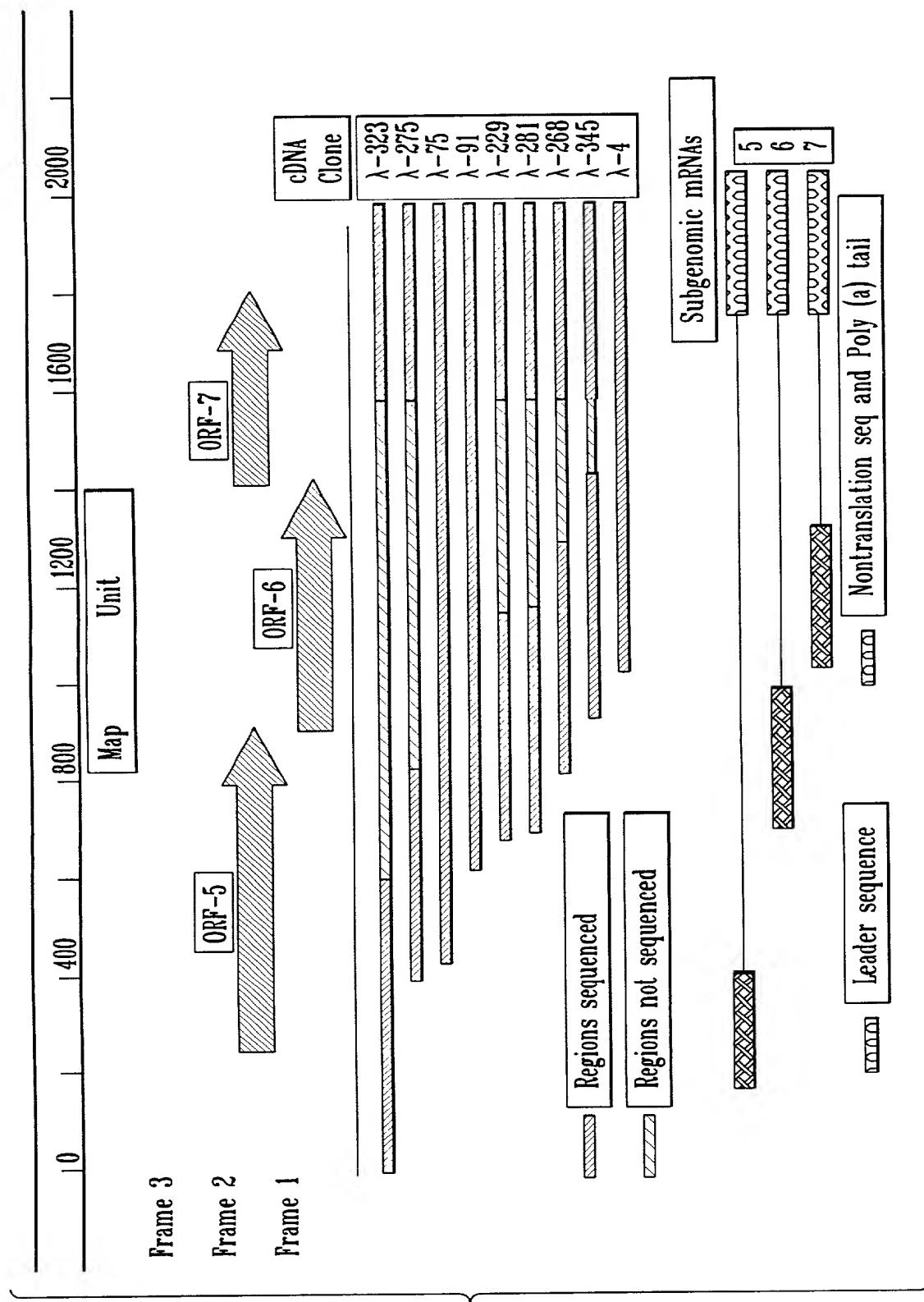


FIG. 5

FIG. 6



GGCAAGGCTTTGGCTGCCTCCAAGACATCAGTGGCTTAGGCATCGGAACCTGGGCCTTGAGGGATTCCGAAAGTCCCCTAGTGGCACGGGATAGGG 100
 ACACCCGTGATA[CACTG]CACAGGCAA[TGT]TACCGAT[GAGAA]TTATT[GCAATTCCCTGATCCTCTAIGCTTCTCTGCCTTTCTATGCTCTG 200
 AGATGAAGTGAAGGGATTAAAGGTTGGATTGGCAATGTTGGCATCTGGCATCTGGCATGTCACCTTACCCAGTTACGTCCAAACATGTCAGGAATT 300
 TACCCAAACGTTCCCTGGTAGTGTGACCATGTTGGGGCTGCTCATTTCATGACGCCGAGACCATGAGGGGGCAACTGAGCTTAAAGCTGCTTTGGCATT 400
 DRF 4 stop
 *** +1>DRF 5 start
CTGTTGGCAATTTGAATGTTAAGTATGTTGGGAAAAGCTTGCTTGACCCGGGGCTGTTGCTCGCAAATGCTTTTGGGGTGTATCGTGGCGTCTGGTTT 500
 GTTGGGCTCGTCAAGGCCAACGGGAACAGGGCAAGGGCTCAAATTACAGCTGATTACAACCTGACGGTAATGTTGACCTAAGGCTAGCTAGGCTAAATA 600
 AATTGACTGGGAGTGGAGTGTTTGCACTGACTCACATGTCCTTATGGTGCCTCACTACTAGCCATTTCCTGACACAGTCGG 700
 TCTGGTCACTGGCTACCGCTGGGTTGTCACGGGGGATGTTGAGTAGGATGTTGAGCTGGCTGGCTGGGTGGAATTGGCTTCGTCATT 800
 AGGCCTGGGAAGAA[TGGATGCTTGCTGGGCTACCTCACTGAACTAATACCAACTTCTCTGGACACTAAGGGAGACTCTATCGTGGGGTGGCTG 900
 TCACTCAAGAGAAAGGGCAAAAGTTGGGGTCAAGGGTCACTGATCACTCAAAAGAGTTGGCTTGAATGGTTCCGGGCTACCCCCGTAACCAGAGT 1000
 DRF 6 start
 +1> ***DRF 5 stop
TTCAGGGAAACAATGGAGTCGTCCTTAGATGACTCTGTCATGATAGCAAGGCTCCACAAAAGGTCCTGGGTTTCTATTACCTACACGGCAGTGA 1100

FIG. 7A

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TGATATGCCCTAAAGGTGAGTCGGGCCGACTGGCTAGGGCTTCTGCACCTTTGGCTTCCAGAATTGGTACATGACATTTCG
 GGACTTTCAAGTAGAAATAAGGTGGGCTCACTATGGGAGCAGTAGTGGACTCTCTGGGGGTGACTCAAGCCATAGAAACCTGGAAATTCAACC
 TCCAGATGCCCTTTGCTTGGTAGGGCAAGTAACATTCTGGCCCTTGCCACACGGTGAAGTGCAGGGCTTCAATCCGATTGGGGAAATGATA
 ACCACGGCATTTGCTCCGGCTCCCACTACGGTCAACGGCACATTGGTGGCCGGTTAAAAGCCCTCGTGTGGGTGGCAGAAAAAGCTGTTAA
 DRF7 start
 +1) ***DRF6 stop
 ACAGGGAGTGGTAAACCTTGTTAAAATGCCAAATAACACGGCAAGCAGGAGAAAGAAGGGGATGGCAGCCAGTCATCAGCTGGCCAGAT
 GCTGGGTAAGATCATCGCTCACCAAAACCAGTCCAGGGCAAGGGACCCTTAATCAAGCCCTTAATCAAGGCGCTGGGACTTCCCTCTAGCG
 ACTGAAGATGAGTGCAAGACATCACTTACCCCTAGTGAGCGTCAATTGCTGCTCAATCCAGGCCCTTAATCAAGGCGCTGGGACTTCCCTCTAGCG
 TGTCAGATTCAAGGGAGGATAAGTTACACTGTGGAGTTAGTTGAAAGAATGGTGGACTGATGACATTGTCGCCTGATCCGGTCAACAGGATCACCCCTCAGGATGATG
 GGCTGGCATTCTGAGGCACTCCAGTGGTGAATTGGAAAGAATGGTGGACTGATGACATTGTCGCCTGATCCGGTCAACAGGATCACCCCTCAGGATGATG
 GACCGTGGGGTAAGATTAAATGGGAGAAACCACAGGGCAAAATTAAAAAA

FIG. 7B

FIG. 8

Year	Deaths	Deaths per 100,000 population	Rate of increase	Rate of decrease	Rate of change	Rate of growth	Rate of decline	Rate of decrease in rate of growth	Rate of growth in rate of decline
1900	1,000,000	10.0	—	—	—	—	—	—	—
1910	1,100,000	11.0	+0.9%	-0.9%	-0.9%	+9.1%	-9.1%	-0.9%	+0.9%
1920	1,200,000	12.0	+8.3%	-8.3%	-8.3%	+8.3%	-8.3%	-8.3%	+8.3%
1930	1,300,000	13.0	+7.7%	-7.7%	-7.7%	+7.7%	-7.7%	-7.7%	+7.7%
1940	1,400,000	14.0	+7.7%	-7.7%	-7.7%	+7.7%	-7.7%	-7.7%	+7.7%
1950	1,500,000	15.0	+6.7%	-6.7%	-6.7%	+6.7%	-6.7%	-6.7%	+6.7%
1960	1,600,000	16.0	+6.0%	-6.0%	-6.0%	+6.0%	-6.0%	-6.0%	+6.0%
1970	1,700,000	17.0	+5.8%	-5.8%	-5.8%	+5.8%	-5.8%	-5.8%	+5.8%
1980	1,800,000	18.0	+5.6%	-5.6%	-5.6%	+5.6%	-5.6%	-5.6%	+5.6%
1990	1,900,000	19.0	+5.2%	-5.2%	-5.2%	+5.2%	-5.2%	-5.2%	+5.2%
2000	2,000,000	20.0	+5.0%	-5.0%	-5.0%	+5.0%	-5.0%	-5.0%	+5.0%
2010	2,100,000	21.0	+4.7%	-4.7%	-4.7%	+4.7%	-4.7%	-4.7%	+4.7%
2020	2,200,000	22.0	+4.3%	-4.3%	-4.3%	+4.3%	-4.3%	-4.3%	+4.3%
2030	2,300,000	23.0	+4.0%	-4.0%	-4.0%	+4.0%	-4.0%	-4.0%	+4.0%
2040	2,400,000	24.0	+3.7%	-3.7%	-3.7%	+3.7%	-3.7%	-3.7%	+3.7%
2050	2,500,000	25.0	+3.4%	-3.4%	-3.4%	+3.4%	-3.4%	-3.4%	+3.4%
2060	2,600,000	26.0	+3.1%	-3.1%	-3.1%	+3.1%	-3.1%	-3.1%	+3.1%
2070	2,700,000	27.0	+2.8%	-2.8%	-2.8%	+2.8%	-2.8%	-2.8%	+2.8%
2080	2,800,000	28.0	+2.5%	-2.5%	-2.5%	+2.5%	-2.5%	-2.5%	+2.5%
2090	2,900,000	29.0	+2.2%	-2.2%	-2.2%	+2.2%	-2.2%	-2.2%	+2.2%
2100	3,000,000	30.0	+1.9%	-1.9%	-1.9%	+1.9%	-1.9%	-1.9%	+1.9%

[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	AA[TGGCACTGG TCGTTAGAT ACTTGTGCA TGA[AGC CTCACAAA AGG[CCCTT -ATGG-GAGG -CGTAGAAG ATT[GCTTAC ACGTACCAA AGC[CGCTT	947 14132
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	GG[GTTCTCT ATTA[CTACA CGGCACTCAT GATA[TGCC CTAAAGTGA GTCGCCG ACGTTAGC ATGAAATTACA GACCTAAAT GATA[GCC CTTAAGCTG CACGCCCG	1007 14192
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	AC[GCTAGGC CTCGGACC [TTTGGCTT CTGAAATTGCTT GGT[TAQQT TCGGTACAT AC[TCGCCC CTTGGACA [CCATAATT TCTGAACCTT TCAATTAGAT TCGATACAT	1067 14252
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	CACA[TCGT CACTTTCA GA[AGAAATAA GSTGGGCTC ACTATGGAC QACTAGTGC CACATATGCA[TTCAAT CCACCAACCC TGTCGACTT ACCTGGGG[TTTGCTG- GATCTTGCTT	1127 14311
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	AC[TCGTTGC CGGGTGTACT CAGG-CATAA GAA[CTGGAA AA[TTATCAC OFCCAGATGC -GCTTGCTT GGGGTGTT CAGGTACACA GASTCATGGA AGTTATCAC TTCCAGATGC	1185 14370
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	GG[GTTGCTT TGC[AGCCCG CAAGTACATT CTGGCCCCTG CCCAC[ACCG] TCAAAGTGCC AGATTGTTT GCG[GGCG GCGATACATT CTGGCCCCTG CCCAT[ACGG] AGAAAGTGGT	1245 14430
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	CCAGGGCTTC A[CCTATTC GGAAATGAT ACCAGCCAT TTTTGTCG CCG[TCGGGC CCAGGCTTC A[TCATTC AGCTCTGGI AACGAGCAT ACCGTCAG AAACCCGA	1305 14490
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	TCAACTACGG TCAACGGCA[ATTGGTCCAC CGCTTAAGAA GCCTCGTGT GCG[TCGGCA CTAACATCG TGAACGGCA[TCAACTACCA CGAQTCCCA CCCTGTCG GCGGGCAAA	1365 14550
[SU 12/7 _a /3' terminal (888 - 1413) Lelystad seq (14077 - 14598)]	AAAGCTGTT AAGAGGGAGT CGTAACCTT GTTAAATAG CGAAATFAA CGAGCTGTT AAGAGGGAGT CCTTAACCTT GTCAACTATG CGGGTAA	1413 14598

FIG. 9

Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	ATGGCCGTA AAAACCGA- AT GATGGCCAGC ATGGCCAG ACCGCAAGC ACCGAAGAG	CAGTCATA AAGAAACT A-CAG---C ACGTGCCAG CAGTCATA AAGAAACT A-CAG---C GCTGTCCAG ATGGCCAGC ATGGCCAG	14681 1434
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	TCGGATGGG AATGGCCAGC CAGTCATA ACTGTGCCAG AAAGGAGGG GATGGCCAGC CAGTCATA GCTGTCCAG	TGGTGGGTG ATGGCCAGC ATGGCCAG GCTGTCCAG ATGGCCAG	14681 1483
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	CAATGATAAA GTCGCCAGGC CAGCAACGTA GGGG-A- -AA-GATCAT CGCTCACCAA AGAACCTGCA GAGCCAGG AAGAAAAATA AGAAGAAAAA	AGAGGCCCAG GCTGTCCAG GTCACCGAC	14728 1528
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	AAGAAAAA----- AAGAAAAATA	-CCTGAGAAG CCACTTTTC CCTCTCCCTGC CCCGAGAAG CCCCATTTCC GTCACCGAC	14766 1578
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	TGAAAGATGAC ATCGGGCAC ACCTCACCCA GACTGAAACCG TGAAAGATGAT GTGAGACATC AGTTTACCC TGAATGAGGT CATATGTC	TCCGTTGCT GAT CCAGGGGT TCAATCAAG GGGCAAAAO TGTCGTDAAAT CCACACGGGC TTAAATCAAG GGGCTGGCAO	14816 1628
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	TGCAAATGAT CCAGGGGT TCAATCAAG GGGCAAAAO TGTCGTDAAAT CCACACGGGC TTAAATCAAG GGGCTGGCAO	TGGCTGGC -TGGTGGC TTGCAAGC-G-C	14865 1677
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	TTCATTCAGC GGGAAAGCTCA GTTTTCAGCT TCACTTTATG CTGGCGCTTG TCACATTCAGC GGGAAAGCTCA GTTTTCAGCT TCACTTTATG CTGGCGCTTG	TGAGTTTACT GTCACATTCAGC GGGAAAGCTCA GTTTTCAGCT TCACTTTATG CTGGCGCTTG TGGCTGGC TTGCAAGC-G-C	14915 1727
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	GTCAATACAGT CCCCTGATT CGCTTGACTT CTACATTCAGC CAGTCAGGCT ATCATACAGT CCCCTGATT CGCTTGACTT CTACATTCAGC CAGTCAGGCT	CTGGCGCTTG TGGCTGGC CTGGCGCTTG CTGGCGCTTG	14965 1774
Leystad seq ISU 12/70/3' terminal (1403 - 1774)	(14588 - 14974)	GCAAGTTAA		14974 1774

FIG. 10

ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	TGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGGA	1814 14976
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AGAA[TGCC]G GTGAAATGCCA C[TGAT]TGADA [TTTG]TCCTCT TGACAG[TCAG] G TGAATGGCC GCGATT[GCG] [CTTG]CCTCT	1854 15016
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAGTCACCTA TTCAATTAGG GCGAACCTGT GGGGTAAAGA GAGTCACCTA TTCAATTAGG GCGATGACAT GGGGTGATA	1800 15056
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	[TTAAAT]GG CGAGAACAC AC[GCGAAA TTAAAAAAA CTTAATCAGG CAGGAACCAT GTGACGAAA TTAAAAAAA	1933 15096
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAAAA AAAAA	1938 15101

FIG. 11

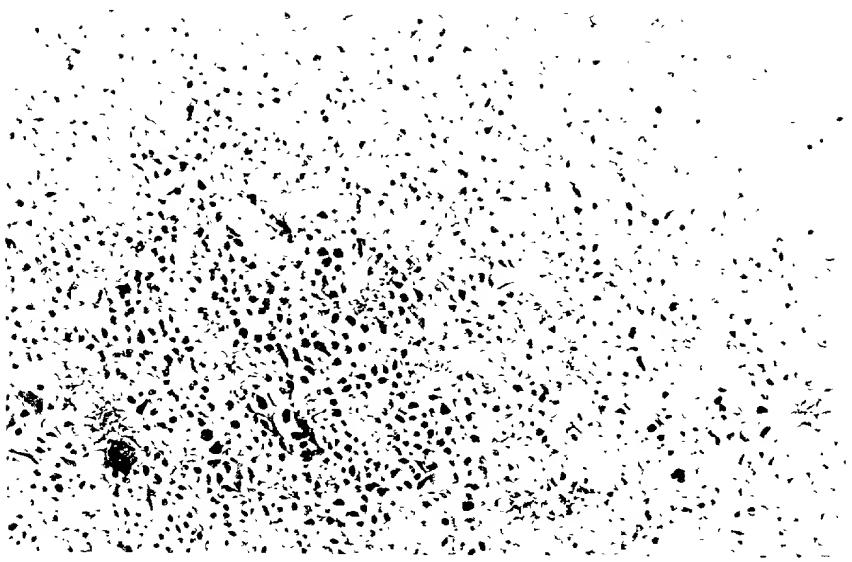


FIG.12

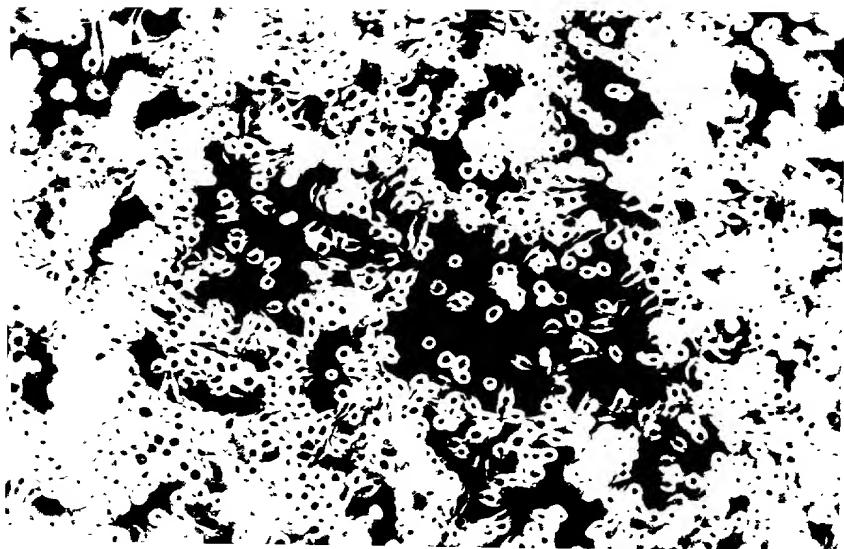


FIG.13

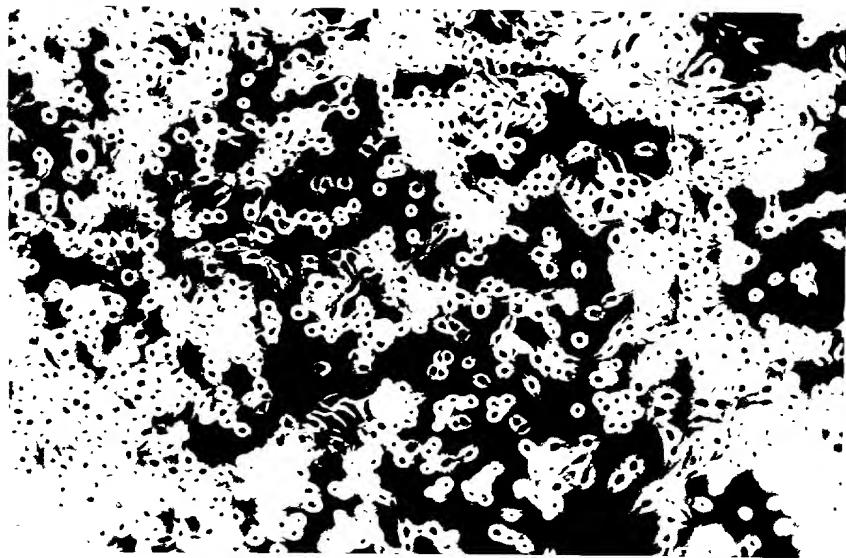


FIG.14

SM E M NP E+M+NP SM

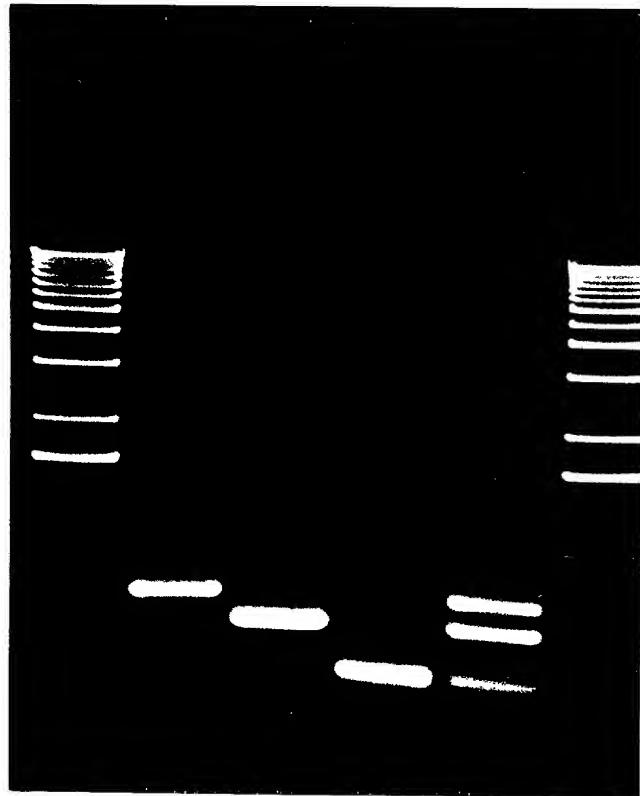


FIG.15

SM pVL1393 E M NP SM

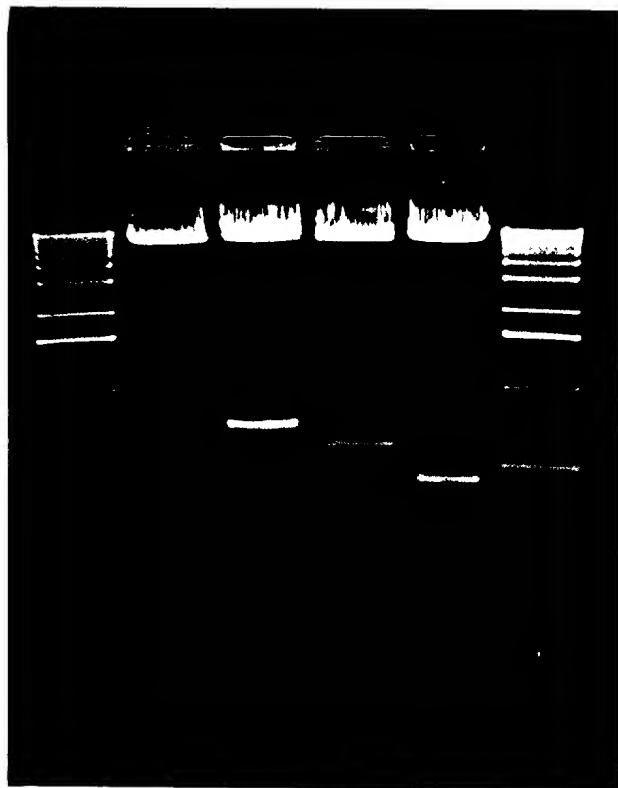


FIG.16

Now, though, the new *Republique* has been established, and the old *Constituent Assembly* dissolved, the *Constituent Assembly* has been succeeded by the *Assembly of the French People*, which is to be the legislative body of the new state.

FIG. 17B

FIG. 17C

VR 2385	CTTGACC-CCTGTCAGATTCAGGAGATAAGTTACACTGGGAGTTAGTTGGCTTAAGGATCATACTGTGGCTGATCCGGTCAAGGATCACCC-	877
ISU-1894	-
ISU-22	-
ISU-79	-
ISU-55	-
ISU-3927	C. T. T. - A. TCCAGC. A. G. C. . TTCAAG. T. TGG. . GGTTCG. A. T. T. A. T. G.	877
LV	-

FIG. 17D

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WR 2385 DRF6 MESSLDIFCHDSTAPQKVLLAFLSITTPVMIYALKVSRGRLGLLHILLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWVYSAIETWKFITSRCR 100
 IISU-1894 DRF6 G.....
 IISU-22 DRF6 G.....
 IISU-55 DRF6 G.....
 IISU-79 DRF6 G.....
 IISU-3927 DRF6 G.....
 LV DRF6 G-G.....
 PRRSV-10 DRF6 G-G.....
 LDV-C DRF2 G-G,-E.....
 LDV-P DRF2 G-G,-E.....

VR 2385	DRF6	LCLLGRKYILAPAHHVESAAAGFHPPIAANDNH-----AFVVVRPGSTTVNGTLVGGRKAVKQGWNLVKY-AK	183
ISU-1894	DRF6	-----	174
ISU-22	DRF6	-----	174
SIU-55	DRF6	-----	174
ISU-79	DRF6	-----	174
ISU-3927	DRF6	-----	174
LV	DRF6	C.....R.....L.....S.....SG.....R.....YA.....K.....L.....S.....R.....KR.....R.....R.....	173
PRRSV-10	DRF6	C.....R.....L.....S.....SG.....R.....YA.....K.....L.....S.....R.....KR.....R.....R.....	173
LDV-C	DRF2	F.....S.....PS.....D-----TSDGRQSLTTSLTT.....K.....L.....Q.....DFQR.....K.....SK.....A.....L.....VS.	171
LDV-P	DRF2	F.....S.....PS.....D-----TSDGRQSLTTSSST.....K.....L.....Q.....DFQR.....K.....SK.....A.....L.....VS.	171

VR 2385	DRF7	MPNNTGKQQKKKK-----GDDQPVNQLCQMLGKIIAHQNQSRGKGPKKNNPEKPHFPLATEDDVRHHFTPSERQLCLSSIQTAFFNQGAGTCTLS	100
ISU-1894	DRF7	N.....	93
ISU-22	DRF7	N.....	93
ISU-79	DRF7	N.....	93
ISU-3927	DRF7	N.....K.....	93
ISU-55	DRF7	N.....K.....	93
VR2332	DRF7	N.....TEE.....	93
LV	DRF7	--A..N..SQ..KKSTAPM..N.....L..AM..KS..R----QPR..GQA..K.....A...I..L..QT..S...Q.....AS..	94
PRRSV-10	DRF7	--A..N..SQ..KKSTAPM..N.....L..AM..KS..R----QPR..GQA..K.....A...I..L..QT..S...Q.....PS..	94
LDV-C	DRF1	SQ..KK..GGQN..-----AN..-----N..LISALLRNAG..--N..K..Q..K..,-Q..-,L..M..GPS..L..VM..N..V..M..R..LV..L....G..Q...V	85
LDV-P	DRF1	SQ..KK..GGQN..-----AN..-----N..LINALLRNAG..--N..K..Q..K..,-Q..-,L..M..GPS..L..VM..N..V..M..R..LV..L....G..Q...V	85
EAV	DRF7	ASRRSRP..ASF-----RN..R--RRQPTSYNDLLRMFG..-----MRVR..PPAQOPTQAI..EPG..L..DLNGQ..ATLS..NV..RF..MI..H..SL..-A	83

VR 2385	DRF7	DSGRISYTVEFLPSTHHTVRLIRVTASP----SA	134
ISU-1894	DRF7	123
ISU-22	DRF7	123
ISU-79	DRF7	123
ISU-3927	DRF7	P, -----	123
ISU-55	DRF7	123
VR2332	DRF7	123
LV	DRF7	S., KV, FQ, . M., VA, STSASQGAS	128
PRRSV-10	DRF7	S., KV, FQ, . M., VA, STSASQGAS	128
LDV-C	DRF1	G, NF, . S, M, . A, NAS, NS-----	115
LDV-P	DRF1	G, NF, . S, M, . A, NAS, NS-----	115
EAV	DRF7	A, GLT, . SW-V, . KQIQ, KVAPP, G, -----	110

FIG. 18B

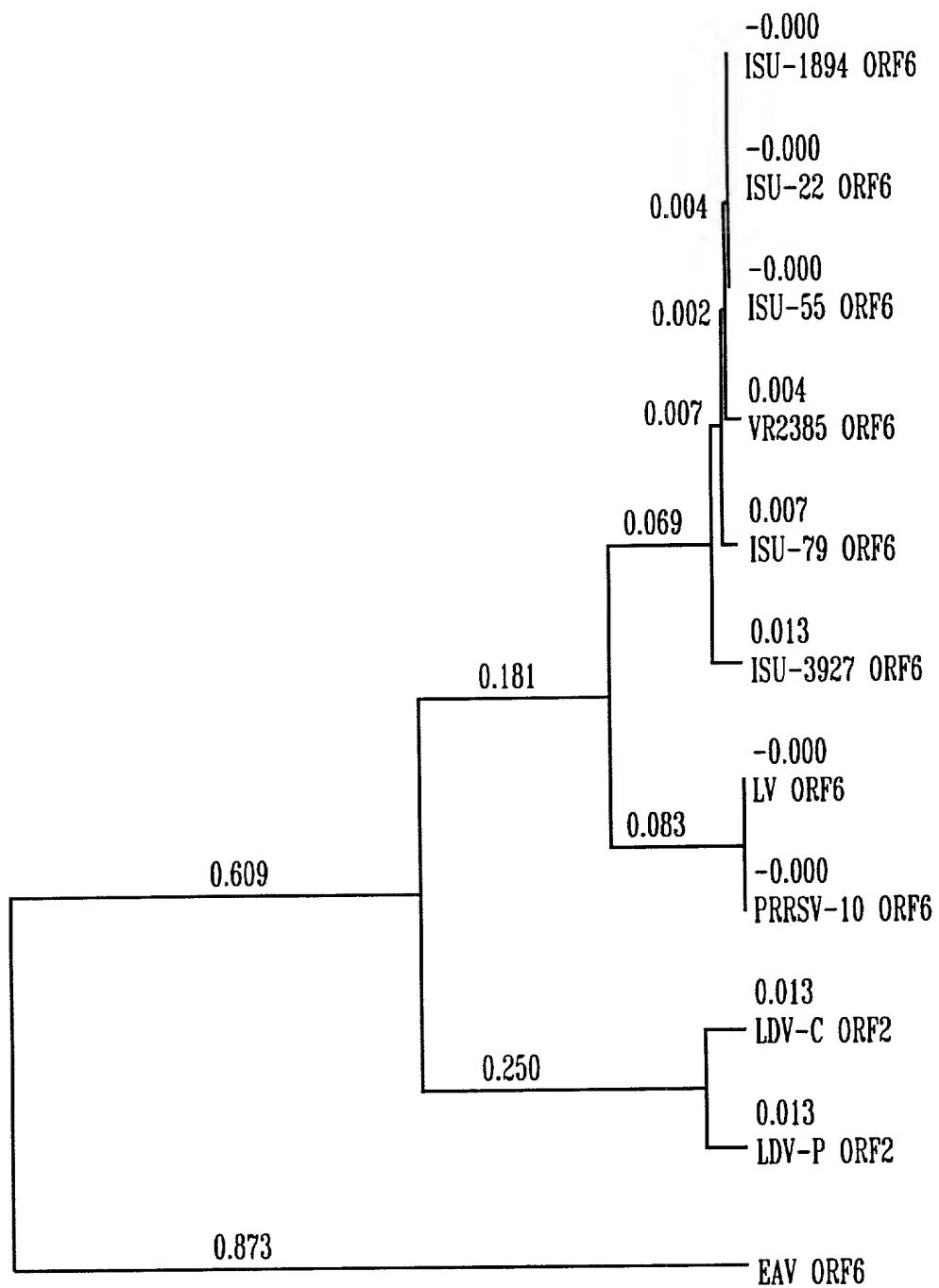


FIG. 19A

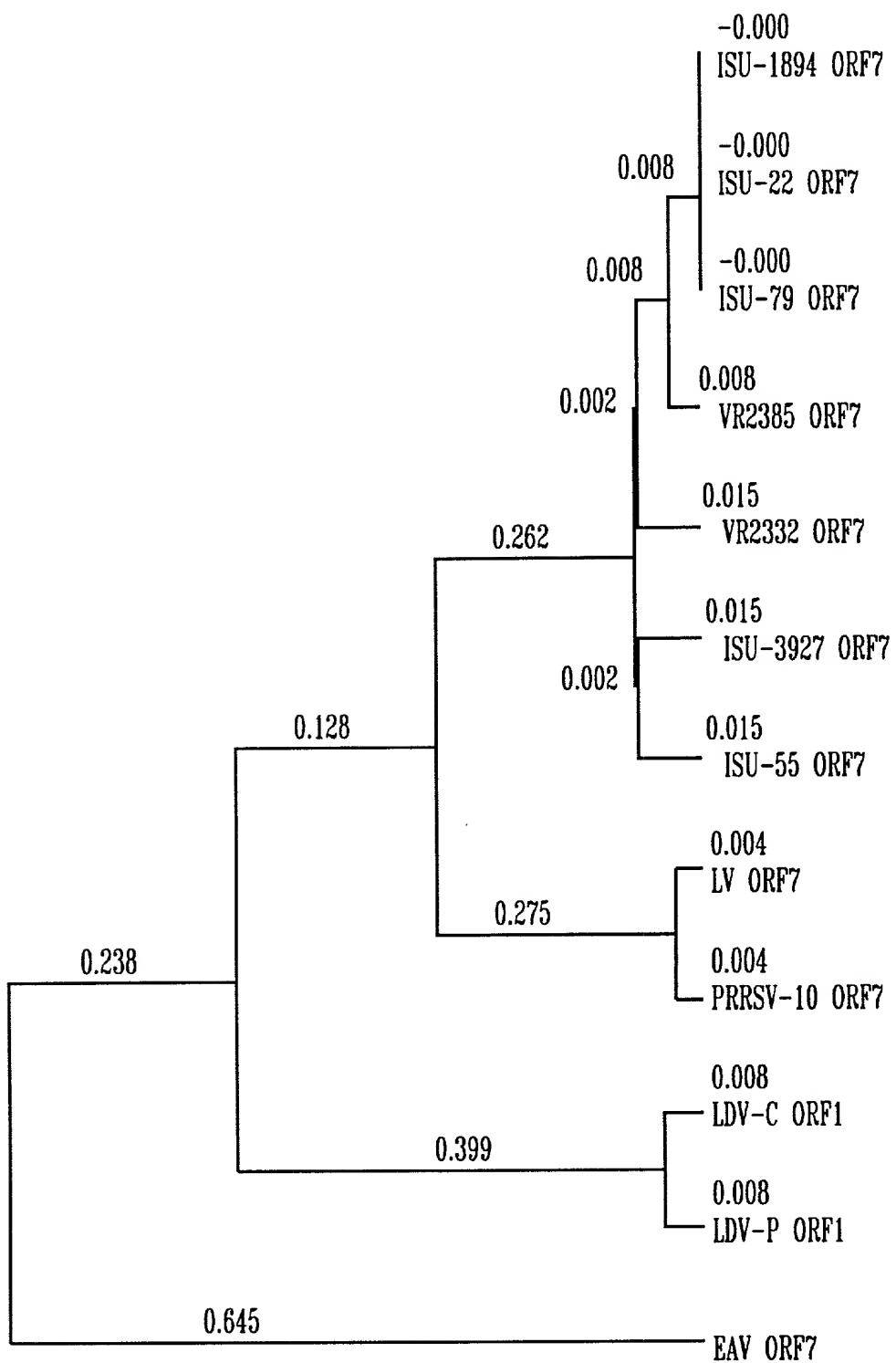


FIG. 19B

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+ Start ORF2	CCTGAATTGAGATGAAATGGGGTCTATGCCAACCTTTTGACAAAATTGGCCAACCTTTTGATGGCTTACGGAGTTCTGGCATTTGTGAT	100
	ATCATATTTGGCCATTGGTTGGCTCACCATCGCAGGTTCTATGCCAACCTTTTGACATTGAGATTGGCTTACGGAGTTCTGGCATTTGTGAT	200
	CTGCCATTCACTTGAGCAATTACAGAAGATCCATTAGGGCCTTCTATGCCAACCTTTTGACATTGAGATTGGCTTACGGAGTTCTGGCATTTGTGAT	300
	TGCTTTGGCACATAAGGGTCAACCCTAGTTGATGAAATGGTGTGAAATGGTGTGAAATGGTACGGCATCATGGAAAAAGCAGGACAGGTGCCTGGAAACAGGT	400
	AGTGAGGGAGGCATACGGCTGTCGGATTAGTAGTTGGATGTGGATGGCTCAATTTCAGGATCTGCCGCCATTGAAGCCGAGACCTGTAATATCTGGCC	500
	TCTCGGCCATGCTACACCACCTGGCATGACAAGGGTCAAATGTAACCATAGTGATAATAGTACTTTGAATCAGGTGTGCTGTTTCCCACCC	600
+ Start ORF3		
	GCTGTGGTTGGTTCCCATGGCTACGTACTGTTTGGTTGGCTGGTTGGCAATTTCGAACTCAGGTGAATTACACGGTGTGCCGC	700
	CTTGGCTCACCGGGCAAGCAGCCACTTGGCATGGGATAGGGATAGGGCATGATCGATGGGGAGGACGATCATGATGAG	800
	ACTAGGGTTGGTGGCCGCTGGCTCTCCAGGAAAGGCCACTTGACAGTGCTTACGGCTGGCTCCCTGTCCTCAGGTATACGGGCCAGTTC	900
	CATCCCCGAGATACTGGGATAGGGAAATGGGAACTTGAGTGAGTGAGCTATGACATCAAGGCCACCAATTCTTGGCCTGTTCAAGCACCCTTGCG	1000
		1100

FIG. 20A

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CCCACCATGACAACATTTCAGCCGTGCCTCAGACCTATTACCAAGCATCAGGTGACGGGGCAATTGGTTTACCTAGAATGGTGCGTCCCCCTTC
 CTCAGGGCTTCTCTGGTTTCAGGGTTCGCCAGGCCATGTTTCAGTCAGTCTGAGTCTCAGACATCAAGACCAACACCCACCGCAG 1300
 + Start DRF 4
 CGGCAAGGCTTTGGTGTCCCTCCAAGACATCAGTTGCCATTAGGCATCGCAACTCGGCCCTCTGAGGGATTGCAAAGTCCCTCAGTGGCACGGGATAGGG 1400
 *** Stop DRF 4
 GACACCCGTGTATAATCACTGTACAGCCAATGTACCAGATGAGAATTATTGGATTTCTCTGATCTCTCATGCTTTCTTGCTTTCTATGCTTCT 1500
 GAGATGAGTGAAAGGGATTAAAGGTGGATTGGCAATTGGTCAAGGTGTGCTCAACTTACCAAGTTACGTCCAAACATGCAAGGAAT 1600
 TTACCCAACGTTCTTGGTAGTTGACCATGTGGCTGCCTCATGACGCCAGACCATGAGGTGGGAACGTGTTAGGCTGTCTTTTACCCAT 1700
 *** Stop DRF 4 + Start DRF 5
 TCTGGGCAATTGGAAATTGGTAAAGTAGTTGGGAAATGCTTACCCGGGGCTGTGCCTGGAAATTGGTGTAACTGGCTTCTGGTGTGCTGGGTGTG 1799

FIG. 20B

Consensus ATGMAATGGGTGCGMTGYRAGCCCTTTGAYAAAATYRGCCARCTKTTYGTTGAYGCYTTCACKGAGTTCYTKGTWSYRTKGTTGATAIYRYATWTT 100
VR2385 D_RF2 ...A.....TA..CAA.....C....TG...A..T..T.....T..T.....G.....T..G..GTCCA..T.....CATT..A.. 100
LV D_RF2 ...C.....AC..TGG..-----T...CA...G..G..C....C..C....T..T.....G..T..TAGTG..G.....TGCC..T.. 91

Consensus YYTKGCCATWYTGTGGSTTACCRCTGGAGGTGGTTRSTGGTCCTTYKYMTCAGAKTGGTTTGCCTGGMWTCCGGTCKCGGCYCTGCCATTCA 200
VR2385 D_RF2 TT..G....TT.....C.....A.....T....C..GG.....T.....TGCA.....T.....A..A.....G.....C..... 200
LV D_RF2 CC..T....AC.....G.....G.....A....T.AC.....CTTC.....G.....C.T.....T.....T.....T..... 191

Consensus TCTSMSAAATYMGAAAGRCCATGARGSCCTTKYTSYCYMASITGMRSSYGGAYAKTCCCACAMTKGSARYYAARCAYCCWTTGGKATGYTTGGCA 300
VR2385 D_RF2 ...GAGC..T..CA...A.....G.C...TC..CT..TC..G...CAGGT..C..T.....-C..GG..G..ACT..A..T..T.....G..C..... 299
LV D_RF2 ...CCCC..C..TC...G.....A.G...GT..GC..CA..C...AGACC..T-G..A..TT..C..GTC..G..C..A....T..T..... 290

Consensus CCATRMGAGTKTCCMMMCYTGGATTGARATGGTSTCKGTCGMAKTKACRSAYCATGGAAMAWKCAAGGCARGCKGCCCTGGAARCAAGGTRGTKRGYGA 400
VR2385 D_RF2 ...AA..-..G..AAC..C.....A.....G..G.....A..G..GC..T.....A..AG..A..G..T.....A..A..GA..C.. 398
LV D_RF2 ...-..GC...T..CCA..T.....G....C..T.....C..T...AG..C.....C..TT...T..A..G.....G..T..TG..T.. 389

Consensus GGCYAUCCGTSTCWCAGMAYWGTCAAGGKVTSGATRTRGTRKRCCTCATTTYCARGCAYCTKGARGCSGAKWCYTGYMRMTWTCRSCTCWCGRGC 500
VR2385 D_RF2 ...T.....G..T..C..TTA..-..-..TT..G...G..GG.....T..G..T.....CA..T..A..C..GA..C..TAAA..A..GGC..T..G.. 496
LV D_RF2 ...C...--..C..A..A..GCT.....GC..C..A..A..TA.....C..A..C..G.....AG..G..G..G..A..C..G.....CAG..A..A..A.. 487

5' >----> 3'
 5' <----< 3'

Consensus	TSSYSATGCTAMAMMAYCTGYCAYGWYAGGGTCAAATGTRASSCMTASWGTYAAYASSYACKTTGRAYCRSGTGTKWGCTCRTYTTCCOMACSCCWGGTV	600
VR2385 ORF2	GCCCC.....C.CC.C...C...T.AC.....A.G.....A.C.A.GT...T..T.GT...T...A.T.AG...T...T...-G.T....A..C..T...T	595
LV ORF2	CGTG.....A.AA.T..-T..-C.TT--.-,-.....G.GC..CA...C..C.CC..G...G.C.GC..-,GA...A.C...C..G..A...A	580
Consensus	CSMGGCCMAAGYTKMNYGATTCTMRCAATGGCTMAATGCTTCCCTCTGKGCKWCWTCKKTACYYTKTTYRTWGTGCTKTG	700
VR2385 ORF2	CC...A...C.TCAT.....CAG.....A.AGC...A..TT.C..T..A.....T..AG.T...TG.T.....G..	695
LV ORF2	GA...C...T.GACC.....AGA.....CAG...G..CG.T..C..T.....G..TT.A..GT..CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTCCARYKCTACGYWMGTGTTGGTTCCRYTGGYMYRSGGCAAYWTCWTTGARCTSACGGTGA	776
VR2385 ORF2	T.G..GG...ATG...TAC.....GC...TTAGG.....TTTT..T.....A..C.....	771
LV ORF2	C.T..AA...GCT...CTA.....AT...CCCAC...CACA..A...G..G...-----	750

FIG. 214. 1

Consensus	ATGGCTMATMRSTGTRCAKCYTCYATWTTTCTCTGTKGCKWKCWTCTKKTACYTKTTYRTWGCTKCTACGTYWMTGTT	100
LV DRF3C.....CAG.....G.....CG.....T.....C.....T.....G.....TT.....A.....GT.....CT.....G.....CA.....AA.....T.....C.....T.....GCT.....AA.....GCT.....CTA.....	100
VR2385 DRF3A.....AGC.....A.....TT.....C.....T.....A.....T.....AG.....T.....TG.....T.....TC.....T.....G.....T.....G.....GG.....T.....TG.....T.....ATG.....T.....TAC.....	100

Consensus	TTTGGTTCCRYTGGYMRSGGCAAYWWTGCTGARCTSACSRSTAAYTACACSRTRTCGMYGCCYGGYYACCMGKCAAUURGCUGLMRARI	200
LV DRF3AT...CCCAC.....CACA..A.....G..CA..C..C.....CA..A.....AT...C..TTCT..A..T.....G.....CA..A..G..	200
VR2385 DRF3GC...TTAGG....TTTT..T.....A..C..GG..G..T.....GG..G..CC...T..CCTC..C..G.....A..-..AG..G..C..	199

Consensus	ACGARCCGGYMGKWMCMTKGGTGCARRATAGGGCATGAYMGRGTGRRGGAGSSRYGAYCATGARYTAGKKWWTGCSRTSCCGTCYGGSYWCKMC	300
LV ORF3	-...G....TC. TAA. A. G....AA.....CA. G....A.....GGT. C.....GT. -..TTAA.....CA. C.....C. .GTA. GA. .	298
VP22385	...REF3.....A.....CA. GTC. C.....GG.....TG. A.....G.....GAC. T.....AC. .GGT.-GG. G.T. .CCT. TC. .	298

Consensus	RCMTATTACCAASCAYCARRTMAGCGGGGCAAATGGTTTCAAGYTRGAATGGSTGGGKCCMTCCTTCTCYTGGYIGGKYMAAYRIMICWgggtTC	600
LV DRF3	G, A.....C, C, AA, A.....C, TT, G.....C, AC.....T, C, C, G, GC, CA, A, A.....	595
VR22385 DRF3	A, C.....G, T, GG, C,.....T, CC, A,.....G, T, CT,.....C, T, T,.....C, T, A,.....TG, C, T,.....	598
Consensus	TSAAGGCCTTCGCCCTGYAAGCCMTGTTCSWSKWCGRMRDTWTCAAGAYATYRAGACCAACACSSACCGCRGKGCAGGTTTGYKGTCCTYCARGACATCART	700
LV DRF3	G,.....T,.....C,.....TCGA, CA,.....A,.....T,.....TG,.....G,.....G,.....T,.....CATG,.....T,.....G,.....A,	695
VR22385 DRF3	C,.....C,.....A,.....AGTT, AG,.....T,.....C, CA,.....G,.....A,.....G,.....A,.....C,.....TGCT,.....C, A,.....G,	698
Consensus	TGYYTYMGRGMCACGGSRWCTORGAGCKCAWGAGRMRATTTCCTTCGSAAAGTGGCYCAGTGGYGAAGSCGGWYRGTACTCCCCAGTAGCATTCAGGA	800
LV DRF3	..TT, CC, A, C,.....GGT, ..A,.....G, ..AAA,.....G, ..G, ..T, ..A, C, ..TCG, ..-.....	795
VR22385 DRF3	..CC, TA, G, A, ..---, CAA, ..G, ..---, T, ---, GCG, ..-.....C, ..-.....C, T, ..G, ..ATA, ..-.....	765

Consensus	TAA	803
LV	DRF3	798
VR2385	DRF3	765

FIG. 21B.1

Consensus	ATGGGTTGCCGCCMYCTTTCYCTGGYTGGTKYTMAAYRTMTCTGGTTCTSAGGGCTTGGCTGYAAGGCOMTGTTCAGAYA	100
VR2385 DRF4G....T..CT.....C..T...T..A..TG..C..T.....C.....A.....C.....A.....C.....A.....C.	100
LV DRF4C....G..AC.....T..C..C...GC..CA..A..A.....G.....T.....C.....TCGA..CA..A.....T.	100
Consensus	TYRAGACCAACACSAACCGCRGCKGCGGGTTTYYKGTGTCCTYCARGACATCARITTGYYTMMGRDMTCAGGESSRWCTCRGCAAGCKCAWGAGRMRATTCCCTT	200
VR2385 DRF4	,CA.....C.....A..G..A..C..TGCT.....C..A.....G..CC..TA..G..A.,---CAA...G.,--T.-T..GCG,-----,	189
LV DRF4	,TG.....G.....G..T..C..T..CATG.....T..G.....A..TT..CC..A.C.....GGT..A..G..A..AAA.....,	200
Consensus	CGSAAAGTCGYCARTGYCGYMRGCSRTMGKAACWCCSWGTAYATCACRKRTMACRGCYAAAGTKACCGAYGARYMMTAYTTGAYWMCKCKGAYCTK	300
VR2385 DRF4	..C.....-C..T..G..C..CAGG..GA..A..G..A..GT..T.....TG..C..A..C..T..T..T..GAAT..T..C..TTC..T..T..T..T	288
LV DRF4	..G.....T..C..A..T..TGAA..CG..C..T..T..CA..C..C..GA..A..G..T..C..G..ATCA..C..T..CAA..G..G..C..G	300
Consensus	CTSATGCTTCTKCKTGGCTTTCTAYGCYTCW GARATGAGYGARAARGGMTTYAARGTSRIMTTGSSAATGTSTCGGCRTYGTKKKCWGYKTGYGTCA	400
VR2385 DRF4	..C.....T..T..G.....T..T..T..G.....T..A..G..A..T..G..GG..A.....C.....G..A..A..C..GG..A..TG..C...	388
LV DRF4	..G.....G..G.....C..C..A..A..C..G..A..C..C..CA..C..G..ATCA..C..T..TT..T..CT..T..T..	400
Consensus	AYTTCACMRRTTAYGTSMMCATGTCAAGGAATTACCCACATACCCAGGAGYATCAYYTGGTARTTGAYCAYRTKCGGYTGCSCATTGCMGACRCC	500
VR2385 DRF4	.C.....CAG..C..CAA.....-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,	476
LV DRF4	.T....AGA..T..GCC..-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,-----,	491
Consensus	MKMKRCMATGAGGTGGGCCWACWRYYWWTGCYTGYTKTYRCATTCTSTIGGAATWTGA	561
VR2385 DRF4	CGAGA..C.....A..TGTII..A..C..C..T..TA..G.....G.....T..	537
LV DRF4	ATCTG..A.....T..AACCA..T..T..T..G..CG.....C.....A..	552

FIG. 21C

Consensus	M. WG. C. K. L. W. L. P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE. L. . . C. . . D. P. . . . KH	100
LV DRF2.	. Q. . H. GV. SASCSWTPS. SSSLV. LI. PF. ---. Y. G. D. Y. F. E. F. P. GL. PN. RP. V. QFAV. .	90
VR2385 DRF2.	. K. . L. --. ---AFLTK. AN-FL. MLSRSSWCP. LI. . . YFW. F. . . A. . . V. W. . . A. D. . . . Y. S. AF. SQ. QV. I. TWGT. .	93
Consensus	PLGM. WH. . VS. LIDEMVSRR. Y. . ME. GQAAWKQVV. EATL. . . S. LD. V. HFQHLAA. EA. . C. . L. SRL. ML. . . . NV. . . . YN. TL. V. . .	200
LV DRF2. F. . MR. H. I. QT. HS. G. TKL. G. . I. T. V. . . DS. RF. S. . . V. . . KN. AV--G. . . SLQ. . T. . . DR. ELJ	188
VR2385 DRF2. L. HK. . T. M. RI. KA. S. . . SRI. S. V. A. I. ET. KY. A. P. HH. RMTGS. . TIV. . S. . . NQ. FAV	193

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Consensus	MA., C., FLC., Y., A., S., T., CFWFPL., GN, SFELT, NYT, C, PC, T, QAA, EPGR, WC, IGHDR, E, DHDEL, PSG, HQ, ARFH, GFIC, LVHS, LASN, SS, L., AH, T., I., I.M., S., S., RQRL, NM., K., E, R., LMSI, YDN	100
LV DRF3.	NS, TFLYI, CSFL, SFCC, VWAG, NA, Y	100
VRR2385 DRF3.	VR, F., V., V.P., L, R., AEAY, SL., R., G, D., GFW, LSS	100

Consensus	...L...YAWLA.LSFSY.AQFHPE.FGIGNVSRV.VD.HQFICA.HDG.N.I....NISA....YY.HQ.DGNNWFHLEW.RP.FSSWVLN.SWL	200
LV DRF3,	L-K.EGY.....F.....A.....L.....F..KR.....E...H..S.VSTGH.....LYAA..H..I.....L..L.....I...	199
VRR2385 DRF3,	EGH.TSA.....S.....T.....Y..IK.....V...Q..T.LPHHD...VLTQ..Q..V.....V..F.....V...	200

Consensus RRSP, S, VS, R, Q, RPT, P, . . . , S, . . . , TS, . . . , L, . . . , R, F, . . . , K, S, . . .
 LV ØRF3, . . . , V, P, . . . , R, IY, IL, . . . , R, RLPVSW, FR, . . . , IVSD, TGQQRK, K, PSESRPNW, P, VLPTSR
 YF223385 ØFE3 . . . , A, H, . . . , V, VE, TS, . . . , P, QRSQAH, L, SK, . . . , V--A, GIAIRPL, R, A-----, LSARR-

FIG. 22B

Consensus	M. A., LF, L, G, . . . , VS, AFACKPCFS, LSDI, TNTTAAAGF, VLQDI, C, R, . . . , A, E, I, . . . , K, . QCR, A, GTP, YIT, TANVTDE, YL, . . . , DL	100
LV DRF4,	, A, AT, . F, A, AQHIM, . E, , TH, . . . , E, , M, , N, F, PHGVSA, Q, K, SFG, SS, . . . , E, V, . . . , Q, . . . , I, , S, . . . , YNA, .	100
YD2205 DRF4	A, S, HR--NS S, A, R--, VP, . . . , T, I, V, . . . , HSS, .	96

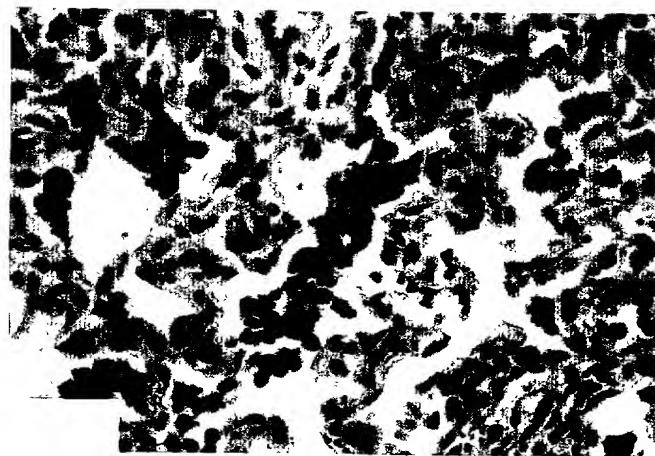


FIG.23

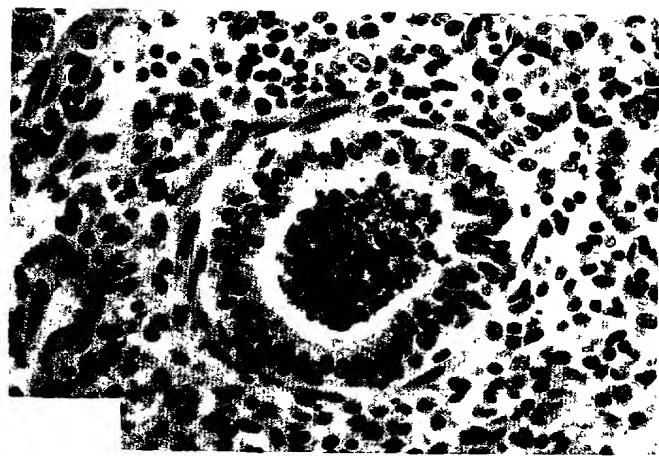


FIG.24

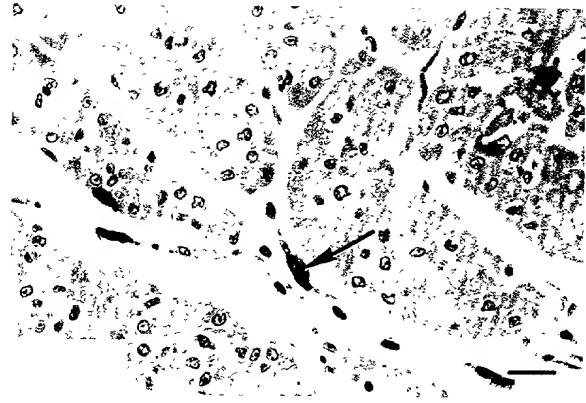


FIG.25

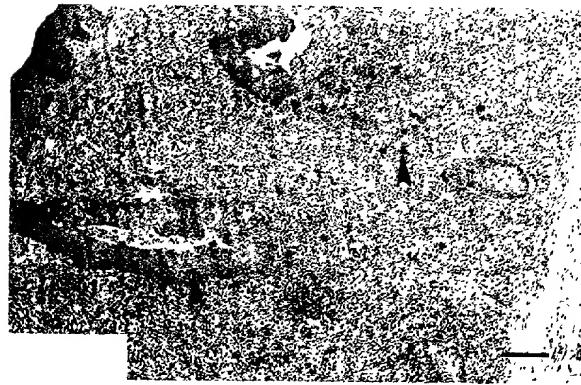


FIG.26

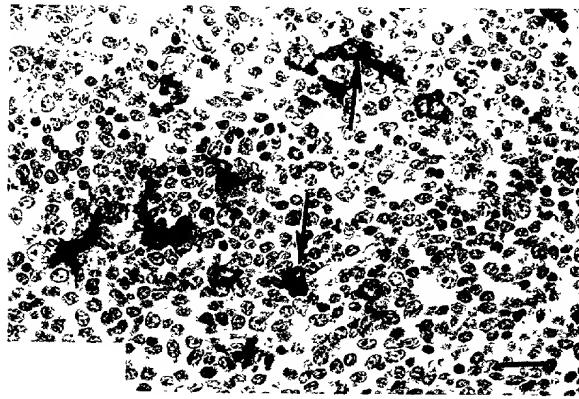


FIG.27



FIG. 28A



FIG. 28B



FIG. 28C

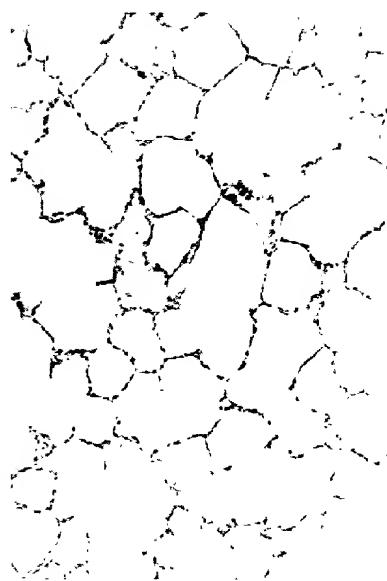


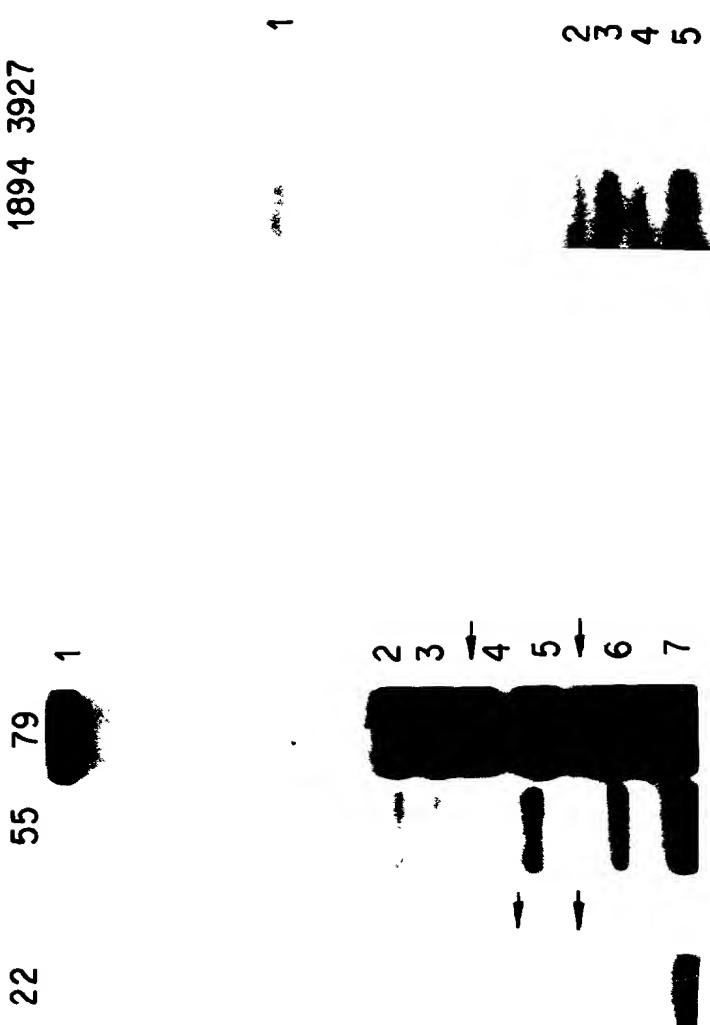
FIG. 29A



FIG. 29B

FIG. 29C

FIG.30A



1894 3927

22 55 79 1

FIG.30B

